Amendment to the Claims

This listing of claims will replace all prior versions and listings of claims.

What Is Claimed Is:

1-10. (Canceled).

11. (Currently Amended) A polypeptide comprising a first amino acid sequence at least 95% identical to a second amino acid sequence selected from the group consisting of:

(a) a full length polypeptide of ~~SEQ ID NO:Y~~ SEQ ID NO: 408 or a full length polypeptide encoded by the HACCI17 cDNA Clone ID in ~~ATCC Deposit No:Z~~ ATCC Deposit No. 203071 corresponding to ~~SEQ ID NO:Y~~ SEQ ID NO: 408 ~~as referenced in Table 1A~~;

(b) a secreted form of ~~SEQ ID NO:Y~~ SEQ ID NO: 408 or a secreted form of the polypeptide encoded by the HACCI17 cDNA Clone ID in ~~ATCC Deposit No:Z~~ ATCC Deposit No. 203071 corresponding to SEQ ID NO: 408 ~~SEQ ID NO:Y as referenced in Table 1A~~;

(c) a polypeptide fragment of at least 30 amino acids of ~~SEQ ID NO:Y~~ SEQ ID NO: 408 or a polypeptide fragment of at least 30 amino acids encoded by the HACCI17 cDNA Clone ID in ~~ATCC Deposit No:Z~~ ATCC Deposit No. 203071 corresponding to SEQ ID NO: 408, ~~SEQ ID NO:Y as referenced in Table 1A~~ wherein said fragment has biological activity;

(d) a polypeptide fragment of at least 50 amino acids of ~~SEQ ID NO:Y~~ SEQ ID NO: 408 or a polypeptide fragment of at least 50 amino acids encoded by the HACCI17 cDNA Clone ID in ~~ATCC Deposit No:Z~~ ATCC Deposit No. 203071 corresponding to ~~SEQ ID NO:Y~~ SEQ ID NO: 408 ~~as referenced in Table 1A~~, wherein said fragment has biological activity;

~~(e) a polypeptide domain of SEQ ID NO:Y as referenced in Table 1B;~~

~~(f) a polypeptide domain of SEQ ID NO:Y as referenced in Table 2; and~~

~~(g) a predicted epitope of SEQ ID NO:Y as referenced in Table 1B.~~

(e) a polypeptide comprising amino acids 1-218 of SEQ ID NO: 408;

(f) a polypeptide comprising amino acids 25-218 of SEQ ID NO: 408; and

(g) a polypeptide comprising the mature form of HACCI17 polypeptide encoded by the HACCI17 cDNA in ATCC Deposit No. 203071.

12. (Previously Presented) The polypeptide of claim 11, wherein said polypeptide comprises a heterologous amino acid sequence.

13. (Previously Presented) The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

14-15. (Canceled).

16. (Currently Amended) ~~A method of making an isolated polypeptide~~ An isolated polypeptide produced by a method comprising:

(a) ~~culturing the recombinant host cell of claim 15 under conditions such that said polypeptide is expressed~~expressing the polypeptide of claim 11 by a cell; and

(b) recovering said polypeptide.

17-19. (Canceled).

20. (Previously Presented) A method of diagnosing diabetes or conditions related to diabetes, or diagnosing susceptibility to diabetes or conditions related to diabetes in a subject comprising:

(a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and

(b) diagnosing diabetes or conditions related to diabetes or the susceptibility to diabetes or conditions related to diabetes based on the presence or amount of expression of the polypeptide.

21. (Currently Amended) A method for identifying a binding partner to the polypeptide of claim 11 comprising:

(a) contacting the polypeptide of claim 11~~43~~ with a binding partner; and

(b) determining whether the binding partner effects an activity of the polypeptide.

22-23. (Canceled)

24. (Currently Amended) The product produced by the method of claim 21~~20~~.

25. (New) A polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) a full length polypeptide of SEQ ID NO: 408 or a full length polypeptide encoded by the HACCI17 cDNA Clone ID in ATCC Deposit No. 203071 corresponding to SEQ ID NO: 408;

(b) a secreted form of SEQ ID NO: 408 or a secreted form of the polypeptide encoded by the HACCI17 cDNA Clone ID in ATCC Deposit No. 203071 corresponding to SEQ ID NO: 408;

(c) a polypeptide fragment of at least 30 amino acids of SEQ ID NO: 408 or a polypeptide fragment of at least 30 amino acids encoded by the HACCI17 cDNA Clone ID in ATCC Deposit No. 203071 corresponding to SEQ ID NO: 408, wherein said fragment has biological activity;

(d) a polypeptide fragment of at least 50 amino acids of SEQ ID NO: 408 or a polypeptide fragment of at least 50 amino acids encoded by the HACCI17 cDNA Clone ID in ATCC Deposit No. 203071 corresponding to SEQ ID NO: 408, wherein said fragment has biological activity;

(e) a polypeptide comprising amino acids 1-218 of SEQ ID NO: 408;

(f) a polypeptide comprising amino acids 25-218 of SEQ ID NO: 408; and

(g) a polypeptide comprising the mature form of HACCI17 polypeptide encoded by the HACCI17 cDNA in ATTC Deposit No. 203071.

26. (New) The polypeptide of claim 25, wherein said polypeptide comprises a heterologous amino acid sequence.

27. (New) The polypeptide of claim 11, wherein said polypeptide is glycosylated.

28. (New) The polypeptide of claim 25, wherein said polypeptide is glycosylated.

29. (New) An isolated polypeptide produced by the method comprising:

(a) expressing the polypeptide of claim 25 by a cell; and

(b) recovering said polypeptide.

30. (New) A method of diagnosing diabetes or conditions related to diabetes, or diagnosing susceptibility to diabetes or conditions related to diabetes in a subject comprising:

(a) determining the presence or amount of expression of the polypeptide of claim 25 in a biological sample; and

(b) diagnosing diabetes or conditions related to diabetes or the susceptibility to diabetes or conditions related to diabetes based on the presence or amount of expression of the polypeptide.

31. (New) A method for identifying a binding partner to the polypeptide of claim 25 comprising:

(a) contacting the polypeptide of claim 25 with a binding partner; and

(b) determining whether the binding partner effects an activity of the polypeptide.

32. (New) The product produced by the method of claim 31.